



PCT/10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/049,957

DATE: 08/30/2002  
TIME: 15:40:25

Input Set : A:\KATO21.txt  
Output Set: N:\CRF4\08302002\J049957.raw

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4 FUJIMOTO, Katsumi
6 <120> TITLE OF INVENTION: CHONDROGENESIS PROMOTERS
8 <130> FILE REFERENCE: KATO=21
10 <140> CURRENT APPLICATION NUMBER: 10/049,957
11 <141> CURRENT FILING DATE: 2002-02-19
13 <150> PRIOR APPLICATION NUMBER: PCT/JS00/05590
14 <151> PRIOR FILING DATE: 2000-08-21
16 <150> PRIOR APPLICATION NUMBER: JP 232966/1999
17 <151> PRIOR FILING DATE: 1999-08-19
19 <160> NUMBER OF SEQ ID NOS: 15
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2388
25 <212> TYPE: DNA
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33 tggaggtgcg gtggtgcacc gcgtccgagc ccgagcagca gaagtgcgag gacatgagcc 180
35 aggccttcgc cgaagccggc ctccagcccg ccctgctgtg cgtgcagggc acctcggccg 240
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85 gccgcaacaa gtgcactggc aacagccagg agcgtacta tggcgacagt ggcgccttca 1740
87 ggtgcctggg ggaggggtgca ggggacgtgg ccttcgtcaa gcacacgacc atctttgaca 1800
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93 agattccgtc ccacgccgtc atggtgcggc ccgacaccaa catcttcacc gtttacggac 1980
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123 Gln Gln Lys Cys Glu Asp Met Ser Gln Ala Phe Arg Glu Ala Gly Leu
124 35 40 45
126 Gln Pro Ala Leu Leu Cys Val Gln Gly Thr Ser Ala Asp His Cys Val
127 50 55 60
129 Gln Leu Ile Ala Ala His Glu Ala Asp Ala Ile Thr Leu Asp Gly Gly
130 65 70 75 80
132 Ala Ile Tyr Glu Ala Gly Lys Glu His Gly Leu Lys Pro Val Val Gly
133 85 90 95
135 Glu Val Tyr Asp Gln Glu Val Gly Thr Ser Tyr Tyr Ala Val Ala Val
136 100 105 110
138 Val Lys Arg Ser Ser Asn Val Thr Ile Asn Thr Leu Arg Gly Val Lys
139 115 120 125
141 Ser Cys His Thr Gly Ile Asn Arg Thr Val Gly Trp Asn Val Pro Val
142 130 135 140
144 Gly Tyr Leu Val Asp Ser Gly Arg Leu Ser Val Met Gly Cys Asp Val
145 145 150 155 160
147 Leu Lys Ala Val Ser Glu Tyr Phe Gly Gly Ser Cys Val Pro Gly Ala
148 165 170 175
150 Gly Glu Thr Arg Tyr Ser Glu Ser Leu Cys Arg Leu Cys Arg Gly Asp
151 180 185 190
153 Thr Ser Gly Glu Gly Val Cys Asp Lys Ser Pro Leu Glu Arg Tyr Tyr
154 195 200 205
156 Asp Tyr Ser Gly Ala Phe Arg Cys Leu Ala Glu Gly Ala Gly Asp Val
157 210 215 220
159 Ala Phe Val Lys His Ser Thr Val Leu Glu Asn Thr Asp Gly Arg Thr
160 225 230 235 240

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162 Leu Pro Ser Trp Gly His Met Leu Met Ser Arg Asp Phe Glu Leu Leu
163      245      250      255
165 Cys Arg Asp Gly Ser Arg Ala Ser Val Thr Glu Trp Gln His Cys His
166      260      265      270
168 Leu Ala Arg Val Pro Ala His Ala Val Val Val Arg Ala Asp Thr Asp
169      275      280      285
171 Ala Gly Leu Ile Phe Arg Leu Leu Asn Glu Gly Gln Arg Leu Phe Ser
172      290      295      300
174 His Glu Gly Ser Ser Phe Gln Met Phe Ser Ser Glu Ala Tyr Gly Gln
175 305      310      315      320
177 Lys Asn Leu Leu Phe Lys Asp Ser Thr Leu Glu Leu Val Pro Ile Ala
178      325      330      335
180 Thr Gln Thr Tyr Glu Ala Trp Leu Gly Pro Glu Tyr Leu His Ala Met
181      340      345      350
183 Lys Gly Leu Leu Cys Asp Pro Asn Arg Leu Pro Pro Tyr Leu Arg Trp
184      355      360      365
186 Cys Val Leu Ser Thr Pro Glu Ile Gln Lys Cys Gly Asp Met Ala Val
187      370      375      380
189 Ala Phe Ser Arg Gln Arg Leu Lys Pro Glu Ile Gln Cys Val Ser Ala
190 385      390      395      400
192 Glu Ser Pro Gln His Cys Met Glu Gln Ile Gln Ala Gly His Ile Asp
193      405      410      415
195 Ala Val Thr Leu Asn Gly Glu Asp Ile His Thr Ala Gly Lys Thr Tyr
196      420      425      430
198 Gly Leu Ile Pro Ala Ala Gly Glu Tyr Ala Ala Asp Asp Arg Ser
199      435      440      445
201 Asn Ser Tyr Phe Val Val Ala Val Val Lys Arg Asp Ser Ala Tyr Ala
202      450      455      460
204 Phe Thr Val Asp Glu Leu Arg Gly Lys Arg Ser Cys His Pro Gly Phe
205 465      470      475      480
207 Gly Ser Pro Ala Gly Trp Asp Val Pro Val Gly Ala Leu Ile His Trp
208      485      490      495
210 Gly Tyr Ile Arg Pro Arg Asn Cys Asp Val Leu Thr Ala Val Gly Gln
211      500      505      510
213 Phe Phe Asn Ala Ser Cys Val Pro Val Asn Asn Pro Lys Lys Tyr Pro
214      515      520      525
216 Ser Ser Leu Cys Ala Leu Cys Val Gly Asp Glu Gln Gly Arg Asn Lys
217      530      535      540
219 Cys Thr Gly Asn Ser Gln Glu Arg Tyr Tyr Gly Asp Ser Gly Ala Phe
220 545      550      555      560
222 Arg Cys Leu Val Glu Gly Ala Gly Asp Val Ala Phe Val Lys His Thr
223      565      570      575
225 Thr Ile Phe Asp Asn Thr Asn Gly His Asn Pro Glu Pro Trp Ala Ala
226      580      585      590
228 His Leu Arg Ser Gln Asp Tyr Glu Leu Leu Cys Pro Asn Gly Ala Arg
229      595      600      605
231 Ala Glu Ala His Gln Phe Ala Ala Cys Asn Leu Ala Gln Ile Pro Ser
232      610      615      620
234 His Ala Val Met Val Arg Pro Asp Thr Asn Ile Phe Thr Val Tyr Gly

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237 Leu Leu Asp Lys Ala Gln Asp Leu Phe Gly Asp Asp His Asn Lys Asn
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240 Gly Phe Lys Met Phe Asp Ser Ser Ser Tyr His Gly Arg Asp Leu Leu
241          660          665          670
243 Phe Lys Asp Ala Thr Val Arg Ala Val Pro Val Gly Glu Arg Thr Thr
244          675          680          685
246 Tyr Gln Asp Trp Leu Gly Pro Asp Tyr Val Ala Ala Leu Glu Gly Met
247          690          695          700
249 Gln Ser Gln Arg Cys Ser Gly Ala Ala Val Gly Ala Pro Gly Ala Ser
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268 gaggccttcc gggaagcggg catccagccc tcctcctctt gcgtccgggg cacctccgcc 240
270 gaccactgcg tccagctcat cgcgccccag gaggtgacg ccatcactct ggatggagga 300
272 gccatctatg aggcgggaaa ggagcacggc ctgaagccgg tggtagggca agtgtagcat 360
274 caagaggtcg gtacctcta ttacgcctg gctgtggtca ggaggagctc ccatgtgacc 420
276 attgacaccg tgaagggcgt gaagtccctg cacacgggca tcaatcgac agtgggctgg 480
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282 tactctgagt cctctgtcgc cctctgcagg ggtgacagct ctggggaagg ggtgtgtgac 660
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328 ctgctggaca aggcccagga cctgttttga gacgaccaca ataagaacgg gttcaaaatg 2040
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357 35 40 45
359 Gln Pro Ser Leu Leu Cys Val Arg Gly Thr Ser Ala Asp His Cys Val
360 50 55 60
362 Gln Leu Ile Ala Ala Gln Glu Ala Asp Ala Ile Thr Leu Asp Gly Gly
363 65 70 75 80
365 Ala Ile Tyr Glu Ala Gly Lys Glu His Gly Leu Lys Pro Val Val Gly
366 85 90 95
368 Glu Val Tyr Asp Gln Glu Val Gly Thr Ser Tyr Tyr Ala Val Ala Val
369 100 105 110
371 Val Arg Arg Ser Ser His Val Thr Ile Asp Thr Leu Lys Gly Val Lys
372 115 120 125
374 Ser Cys His Thr Gly Ile Asn Arg Thr Val Gly Trp Asn Val Pro Val
375 130 135 140
377 Gly Tyr Leu Val Glu Ser Gly Arg Leu Ser Val Met Gly Cys Asp Val
378 145 150 155 160
380 Leu Lys Ala Val Ser Asp Tyr Phe Gly Gly Ser Cys Val Pro Gly Ala
381 165 170 175
383 Gly Glu Thr Ser Tyr Ser Glu Ser Leu Cys Arg Leu Cys Arg Gly Asp
384 180 185 190
386 Ser Ser Gly Glu Gly Val Cys Asp Lys Ser Pro Leu Glu Arg Tyr Tyr
387 195 200 205
389 Asp Tyr Ser Gly Ala Phe Arg Cys Leu Ala Glu Gly Ala Gly Asp Val
390 210 215 220
392 Ala Phe Val Lys His Ser Thr Val Leu Glu Asn Thr Asp Gly Lys Thr
393 225 230 235 240
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VERIFICATION SUMMARY

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